

#09

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## RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/935,799A

TIME: 12:47:44

Input Set : A:\032301.195.seq.ST25.txt

Output Set: N:\CRF3\02212002\I935799A.raw

ENTERED

3 <110> APPLICANT: MOCKEL, Bettina, et al.  
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE csta GENE  
 7 <130> FILE REFERENCE: 032301 WD 195  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/935,799A  
 C--> 9 <141> CURRENT FILING DATE: 2002-02-07  
 9 <160> NUMBER OF SEQ ID NOS: 7  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 2718  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Corynebacterium glutamicum  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (200)..(2515)  
 21 <223> OTHER INFORMATION:  
 24 <400> SEQUENCE: 1

25	aggatggtat aaatcatctc tcaatgttac ttttccattg ttaagaatta acaactctcg	60
27	gtgatttgtc gcatacccag ctgtcaaaga tccgatcatc ggcatacaga aacacccatc	120
29	tggccgaact ttcctttttc tgcattgcatt tctgcacaca gtttctgccc gctgtttctg	180
31	cccgtgttt ctacgcata gtg gct ttg aaa cga ccc gaa gag aaa aca gta	232
32	Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val	
33	1 5 10	
35	aag atc gtg acc ata aaa cag act gac aac atc aat gac gat gat ttg	280
36	Lys Ile Val Thr Ile Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu	
37	15 20 25	
39	gtg tac agc aac gct act gac ctt cca gta ggc gtg aag aag tcc cct	328
40	Val Tyr Ser Asn Ala Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro	
41	30 35 40	
43	aaa atg tca ccg acc gcc cgc gtt ggt ctc ctt gtc ttt ggg gtt atc	376
44	Lys Met Ser Pro Thr Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile	
45	45 50 55	
47	gcg gcg gtg ggt tgg gga gca atc gct ttc tcc cgt ggc gaa aca atc	424
48	Ala Ala Val Gly Trp Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile	
49	60 65 70 75	
51	aac tct gtg tgg ctg gtt ttg gcg gca gtt ggt tcc tat atc att gcg	472
52	Asn Ser Val Trp Leu Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala	
53	80 85 90	
55	ttt tct ttc tat gcc cga ctg att gaa tac aaa gtt gtt aag ccg aaa	520
56	Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys	
57	95 100 105	
59	gat cag cga gca acc ccg gcg gaa tac gtt aat gac ggc aag gac tat	568
60	Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr	
61	110 115 120	

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63 gtc cca acg gat cgt cgt gtg ctt ttt ggc cac cac ttt gca gct att      616
64 Val Pro Thr Asp Arg Arg Val Leu Phe Gly His His Phe Ala Ala Ile
65      125                      130                      135
67 gca ggt gcc ggt cca ttg gtt gga cct gtc atg gcc gcg cag atg ggc      664
68 Ala Gly Ala Gly Pro Leu Val Gly Pro Val Met Ala Ala Gln Met Gly
69 140                      145                      150                      155
71 tac ctg cca ggc acc ttg tgg att atc ctc ggt gtg att ttc gcc ggt      712
72 Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly
73      160                      165                      170
75 gca gtg cag gac tac cta gtg ctg tgg gtg tct act cgt agg cgt gga      760
76 Ala Val Gln Asp Tyr Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly
77      175                      180                      185
79 cgc tca ctt ggc cag atg gtt cgt gat gaa atg ggc acg gtc ggt gga      808
80 Arg Ser Leu Gly Gln Met Val Arg Asp Glu Met Gly Thr Val Gly Gly
81      190                      195                      200
83 gct gcc ggt atc ttg gcg acc atc tcc atc atg atc atc att atc gcg      856
84 Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala
85      205                      210                      215
87 gtg ctc gca ttg atc gtg gtt aat gca ctg gct gat tca cca tgg ggc      904
88 Val Leu Ala Leu Ile Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly
89 220                      225                      230                      235
91 gtt ttc tcc atc acc atg acc atc cca att gca ctg ttc atg ggt gtg      952
92 Val Phe Ser Ile Thr Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val
93      240                      245                      250
95 tac ttg cgt tac ctg cgc cca ggt cgt gtt act gaa gtg tcc atc atc      1000
96 Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile
97      255                      260                      265
99 ggt gtg gca ctg ctc ctg ctg gct atc gtt gct ggt ggt tgg gtt gca      1048
100 Gly Val Ala Leu Leu Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala
101      270                      275                      280
103 gac acc tca tgg ggc gtg gaa tgg ttc acc tgg tct aag acc act ttg      1096
104 Asp Thr Ser Trp Gly Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu
105      285                      290                      295
107 gcg ttg gcc ttg atc ggt tac gga atc atg gct gcg att ttg ccg gtg      1144
108 Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val
109 300                      305                      310                      315
111 tgg ctg ctg ctt gca ccg cgc gat tac ctg tct acc ttt atg aag atc      1192
112 Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile
113      320                      325                      330
115 ggc gtc atc ggt ctg ttg gca gtg ggt att ttg ttc gca cgt cct gag      1240
116 Gly Val Ile Gly Leu Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu
117      335                      340                      345
119 gtg cag atg cct tcc gtg acc tcc ttc gca ctt gag ggc aac ggt ccg      1288
120 Val Gln Met Pro Ser Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro
121      350                      355                      360
123 gtg ttc tct gga agt ctg ttc cca ttc ctg ttc atc acg att gcc tgt      1336
124 Val Phe Ser Gly Ser Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys
125      365                      370                      375
127 ggt gca ctg tct ggt ttc cac gca ctg att tct tca gga acc aca cca      1384

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128	Gly	Ala	Leu	Ser	Gly	Phe	His	Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	
129	380					385					390					395	
131	aag	ctt	gtg	gag	aag	gaa	tcc	cag	atg	cgc	atg	ctc	ggc	tac	ggc	ggc	1432
132	Lys	Leu	Val	Glu	Lys	Glu	Ser	Gln	Met	Arg	Met	Leu	Gly	Tyr	Gly	Gly	
133					400					405					410		
135	atg	ttg	atg	gaa	tct	ttc	gtg	gcg	atg	atg	gca	ctg	atc	acc	gct	gtt	1480
136	Met	Leu	Met	Glu	Ser	Phe	Val	Ala	Met	Met	Ala	Leu	Ile	Thr	Ala	Val	
137					415					420					425		
139	att	ctg	gat	cgt	cac	ctg	tac	ttc	tcc	atg	aac	gct	ccg	ctg	gca	ctg	1528
140	Ile	Leu	Asp	Arg	His	Leu	Tyr	Phe	Ser	Met	Asn	Ala	Pro	Leu	Ala	Leu	
141				430					435					440			
143	act	ggt	gga	gat	cca	gca	acc	gca	gct	gag	tgg	gtt	aac	tcc	att	ggg	1576
144	Thr	Gly	Gly	Asp	Pro	Ala	Thr	Ala	Ala	Glu	Trp	Val	Asn	Ser	Ile	Gly	
145		445					450						455				
147	ctg	aca	ggt	gcg	gat	atc	acc	ccg	gaa	cag	ctg	tcg	gaa	gct	gct	gaa	1624
148	Leu	Thr	Gly	Ala	Asp	Ile	Thr	Pro	Glu	Gln	Leu	Ser	Glu	Ala	Ala	Glu	
149	460					465				470						475	
151	agt	gtc	gga	gaa	tcc	act	gtt	att	tcc	cgt	acc	ggg	ggc	gca	cca	acc	1672
152	Ser	Val	Gly	Glu	Ser	Thr	Val	Ile	Ser	Arg	Thr	Gly	Gly	Ala	Pro	Thr	
153					480					485						490	
155	ttg	gcg	ttc	ggt	atg	tct	gaa	atc	ctc	tcc	gga	ttc	atc	ggc	ggc	gct	1720
156	Leu	Ala	Phe	Gly	Met	Ser	Glu	Ile	Leu	Ser	Gly	Phe	Ile	Gly	Gly	Ala	
157				495						500					505		
159	gga	atg	aag	gcg	ttc	tgg	tac	cac	ttc	gcc	atc	atg	ttt	gag	gct	ctg	1768
160	Gly	Met	Lys	Ala	Phe	Trp	Tyr	His	Phe	Ala	Ile	Met	Phe	Glu	Ala	Leu	
161			510					515					520				
163	ttc	atc	ctc	act	act	gtg	gat	gca	ggt	act	cgt	gtg	gct	cgc	ttt	atg	1816
164	Phe	Ile	Leu	Thr	Thr	Val	Asp	Ala	Gly	Thr	Arg	Val	Ala	Arg	Phe	Met	
165		525						530					535				
167	atg	acc	gat	acc	ttg	ggc	aat	gtt	cca	ggt	ctg	cgc	cgt	ttc	aag	gat	1864
168	Met	Thr	Asp	Thr	Leu	Gly	Asn	Val	Pro	Gly	Leu	Arg	Arg	Phe	Lys	Asp	
169	540					545					550					555	
171	cct	tca	tgg	act	gtc	ggt	aac	tgg	att	tct	acc	gtg	ttt	gtg	tgt	gct	1912
172	Pro	Ser	Trp	Thr	Val	Gly	Asn	Trp	Ile	Ser	Thr	Val	Phe	Val	Cys	Ala	
173					560					565					570		
175	cta	tgg	ggt	gct	att	ttg	ctc	atg	ggt	gtt	acc	gat	cca	ctg	ggc	ggc	1960
176	Leu	Trp	Gly	Ala	Ile	Leu	Leu	Met	Gly	Val	Thr	Asp	Pro	Leu	Gly	Gly	
177				575					580					585			
179	atc	aac	gtg	ctt	ttc	cca	cta	ttc	ggt	atc	gct	aac	cag	ctg	ctc	gcc	2008
180	Ile	Asn	Val	Leu	Phe	Pro	Leu	Phe	Gly	Ile	Ala	Asn	Gln	Leu	Leu	Ala	
181			590					595						600			
183	gct	att	gca	ctt	gct	ctc	gtg	ctg	gtt	gtt	gtg	gtg	aag	aag	ggc	ctg	2056
184	Ala	Ile	Ala	Leu	Ala	Leu	Val	Leu	Val	Val	Val	Val	Lys	Lys	Gly	Leu	
185		605					610						615				
187	tac	aag	tgg	gcg	tgg	att	cca	gct	gtt	cct	ttg	gca	tgg	gat	ctc	att	2104
188	Tyr	Lys	Trp	Ala	Trp	Ile	Pro	Ala	Val	Pro	Leu	Ala	Trp	Asp	Leu	Ile	
189	620					625					630					635	
191	gtc	acg	atg	act	gcg	tca	tgg	cag	aag	att	ttc	cac	tct	gat	ccg	gct	2152
192	Val	Thr	Met	Thr	Ala	Ser	Trp	Gln	Lys	Ile	Phe	His	Ser	Asp	Pro	Ala	

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193          640          645          650
195 att ggc tac tgg gct cag aac gcg aac ttc cgc gat gca aag tct caa      2200
196 Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln
197          655          660          665
199 ggc ctt acc gaa ttt ggt gcc gct aaa tct cct gag gca atc gat gcg      2248
200 Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala
201          670          675          680
203 gtt atc cga aac acc atg att cag ggc atc ttg tcc atc ctg ttc gcg      2296
204 Val Ile Arg Asn Thr Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala
205          685          690          695
207 gtg ctc gtc ctc gtt gtt gtc ggc gca gcc att gcg gtg tgc atc aag      2344
208 Val Leu Val Leu Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys
209 700          705          710          715
211 tcc atc agg gct cgt gca gcc gga aca cct ttg gag acc act gaa gag      2392
212 Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu
213          720          725          730
215 cct gat act gaa tct gag ttc ttc gcc cca act gga ttc ctt gca tct      2440
216 Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser
217          735          740          745
219 tcc agg gat aag gaa gtc cag gcc atg tgg gac gag cgc tac cca gcc      2488
220 Ser Arg Asp Lys Glu Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly
221          750          755          760
223 ggt gcg ccc gtg tct tct gga ggg cac taaaacatga tggctcttac      2535
224 Gly Ala Pro Val Ser Ser Gly Gly His
225          765          770
227 tcatgcactg tggaaaatcc cgcggggcggt gtggtggtat ctcaactgagc tcatggggga      2595
229 cacggcgtat tccaagtatg tgggtgcactt aaagcaccac catccggatg ctccgattcc      2655
231 tactgagcgg gagtattggc gggcaaagta tgcagatcag gacgctaatc ctggtgcccg      2715
233 ctg      2718
236 <210> SEQ ID NO: 2
237 <211> LENGTH: 772
238 <212> TYPE: PRT
239 <213> ORGANISM: Corynebacterium glutamicum
241 <400> SEQUENCE: 2
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247 Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala
248          20          25          30
251 Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
252          35          40          45
255 Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
256          50          55          60
259 Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
260 65          70          75          80
263 Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
264          85          90          95
267 Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
268          100          105          110
271 Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg

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272      115      120      125
275 Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
276      130      135      140
279 Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
280 145      150      155      160
283 Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
284      165      170      175
287 Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
288      180      185      190
291 Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
292      195      200      205
295 Ala Thr Ile Ser Ile Met Ile Ile Ile Ala Val Leu Ala Leu Ile
296      210      215      220
299 Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
300 225      230      235      240
303 Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
304      245      250      255
307 Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
308      260      265      270
311 Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
312      275      280      285
315 Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
316      290      295      300
319 Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
320 305      310      315      320
323 Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
324      325      330      335
327 Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
328      340      345      350
331 Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
332      355      360      365
335 Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
336      370      375      380
339 Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
340 385      390      395      400
343 Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
344      405      410      415
347 Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
348      420      425      430
351 Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
352      435      440      445
355 Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
356      450      455      460
359 Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
360 465      470      475      480
363 Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
364      485      490      495
367 Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
368      500      505      510

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date